

RAW SEQUENCE LISTING

DATE: 01/30/2002

PATENT APPLICATION: US/09/993,346

TIME: 17:24:49

Input Set : N:\Crif3\RULE60\09993346.txt

Output Set: N:\CRF3\01302002\I993346.raw

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65          (A) TELEPHONE: (650) 324-0880
66          (B) TELEFAX: (650) 324-0960
69 (2) INFORMATION FOR SEQ ID NO: 1:
71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 42 base pairs
73          (B) TYPE: nucleic acid
74          (C) STRANDEDNESS: double
75          (D) TOPOLOGY: linear
77      (ii) MOLECULE TYPE: DNA (genomic)
79      (iii) HYPOTHETICAL: NO
81      (vi) ORIGINAL SOURCE:
82          (C) INDIVIDUAL ISOLATE: Human ferredoxin gene
85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
87 GCTCTGCTTG CCAATGTCTT TATAGGTCAC CCGGAAGGCA CG          42
89 (2) INFORMATION FOR SEQ ID NO: 2:
91      (i) SEQUENCE CHARACTERISTICS:
92          (A) LENGTH: 44 base pairs
93          (B) TYPE: nucleic acid
94          (C) STRANDEDNESS: double
95          (D) TOPOLOGY: linear
97      (ii) MOLECULE TYPE: DNA (genomic)
99      (iii) HYPOTHETICAL: NO
W--> 102      (iv) ANTI-SENSE: Human macrophage alpha-antitrypsin
101      (vi) ORIGINAL SOURCE:
105      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
107 CCTACTGCCT CCACCCGAAG TCTACTTCCT GGGTGGGCAG GAAC          44
-----
109 (2) INFORMATION FOR SEQ ID NO: 3:
111      (i) SEQUENCE CHARACTERISTICS:
112          (A) LENGTH: 46 base pairs
113          (B) TYPE: nucleic acid
114          (C) STRANDEDNESS: double
115          (D) TOPOLOGY: linear
117      (ii) MOLECULE TYPE: DNA (genomic)
119      (iii) HYPOTHETICAL: NO
121      (vi) ORIGINAL SOURCE:
122          (C) INDIVIDUAL ISOLATE: Human gene B for alpha 1-acid
123                                  glycoprotein
126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
128 AGTGACCGCC CATAGTTTAT TATAAAGGTG ACTGCACCTT GCAGCC          46
130 (2) INFORMATION FOR SEQ ID NO: 4:
132      (i) SEQUENCE CHARACTERISTICS:
133          (A) LENGTH: 47 base pairs
134          (B) TYPE: nucleic acid
135          (C) STRANDEDNESS: double
136          (D) TOPOLOGY: linear
138      (ii) MOLECULE TYPE: DNA (genomic)
140      (iii) HYPOTHETICAL: NO
142      (vi) ORIGINAL SOURCE:
143          (C) INDIVIDUAL ISOLATE: Human gene for alpha 1

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144                                     microtubulin-bikunin
147      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
149 ATTGGAGCTG TCCTTGGGGC TGTAATTGGC CCCAGCTGAG CAGGGCA      47
151 (2) INFORMATION FOR SEQ ID NO: 5:
153      (i) SEQUENCE CHARACTERISTICS:
154          (A) LENGTH: 45 base pairs
155          (B) TYPE: nucleic acid
156          (C) STRANDEDNESS: double
157          (D) TOPOLOGY: linear
159      (ii) MOLECULE TYPE: DNA (genomic)
161      (iii) HYPOTHETICAL: NO
163      (vi) ORIGINAL SOURCE:
164          (C) INDIVIDUAL ISOLATE: Human gene for alpha-2 macroglobulin
167      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
169 CTGTTTGCAC ACAGAGCAGC ATAAAGCCCA GTTGCTTTGG GAAGT      45
171 (2) INFORMATION FOR SEQ ID NO: 6:
173      (i) SEQUENCE CHARACTERISTICS:
174          (A) LENGTH: 48 base pairs
175          (B) TYPE: nucleic acid
176          (C) STRANDEDNESS: double
177          (D) TOPOLOGY: linear
179      (ii) MOLECULE TYPE: DNA (genomic)
181      (iii) HYPOTHETICAL: NO
183      (vi) ORIGINAL SOURCE:
184          (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal
185                                     3-oxoacyl-CoA
188      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
190 CTCGGGTTTG GCTACAAAAG GTGGAAAGAC TTCCGGTCTG CATTTCTG      48
192 (2) INFORMATION FOR SEQ ID NO: 7:
194      (i) SEQUENCE CHARACTERISTICS:
195          (A) LENGTH: 48 base pairs
196          (B) TYPE: nucleic acid
197          (C) STRANDEDNESS: double
198          (D) TOPOLOGY: linear
200      (ii) MOLECULE TYPE: DNA (genomic)
202      (iii) HYPOTHETICAL: NO
204      (vi) ORIGINAL SOURCE:
205          (C) INDIVIDUAL ISOLATE: Human ACAA gene for peroxisomal
206                                     3-oxoacyl-CoA
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
211 CAAGGTAGGC GGGGCATTGA GTGGAAAGCT CGGCTGGGCG GTGCCTGT      48
213 (2) INFORMATION FOR SEQ ID NO: 8:
215      (i) SEQUENCE CHARACTERISTICS:
216          (A) LENGTH: 48 base pairs
217          (B) TYPE: nucleic acid
218          (C) STRANDEDNESS: double
219          (D) TOPOLOGY: linear
221      (ii) MOLECULE TYPE: DNA (genomic)
223      (iii) HYPOTHETICAL: NO

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225 (vi) ORIGINAL SOURCE:
226 (C) INDIVIDUAL ISOLATE: Human choline acetyltransferase gene
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
231 GCAATTGTGA CCCACAGCCT AATAATAACA GTCTTTGCC TCTTGCC 48
233 (2) INFORMATION FOR SEQ ID NO: 9:
235 (i) SEQUENCE CHARACTERISTICS:
236 (A) LENGTH: 45 base pairs
237 (B) TYPE: nucleic acid
238 (C) STRANDEDNESS: double
239 (D) TOPOLOGY: linear
241 (ii) MOLECULE TYPE: DNA (genomic)
243 (iii) HYPOTHETICAL: NO
245 (vi) ORIGINAL SOURCE:
246 (C) INDIVIDUAL ISOLATE: Human angiotensin I-converting
247 enzyme gene
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
252 GCGGGGGTG TGTGCGGTTT TATAACCCGC AGGGCGGCCG CGGCG 45
254 (2) INFORMATION FOR SEQ ID NO: 10:
256 (i) SEQUENCE CHARACTERISTICS:
257 (A) LENGTH: 45 base pairs
258 (B) TYPE: nucleic acid
259 (C) STRANDEDNESS: double
260 (D) TOPOLOGY: linear
262 (ii) MOLECULE TYPE: DNA (genomic)
264 (iii) HYPOTHETICAL: NO
266 (vi) ORIGINAL SOURCE:
267 (C) INDIVIDUAL ISOLATE: Human gene fragment for the
268 acetylcholine receptor gamma
271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
273 GGGGTGGGAG TGTAGGCTGT TATATGACAC CCAGAGCCCA TCTCT 45
275 (2) INFORMATION FOR SEQ ID NO: 11:
277 (i) SEQUENCE CHARACTERISTICS:
278 (A) LENGTH: 46 base pairs
279 (B) TYPE: nucleic acid
280 (C) STRANDEDNESS: double
281 (D) TOPOLOGY: linear
283 (ii) MOLECULE TYPE: DNA (genomic)
285 (iii) HYPOTHETICAL: NO
287 (vi) ORIGINAL SOURCE:
288 (C) INDIVIDUAL ISOLATE: Human cytokine (Act-2) gene
291 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
293 GTCCTAGGCC TCAGAGTCCC TATAAAGAGA GATTCCAAC TCAGTA 46
295 (2) INFORMATION FOR SEQ ID NO: 12:
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 45 base pairs
299 (B) TYPE: nucleic acid
300 (C) STRANDEDNESS: double
301 (D) TOPOLOGY: linear
303 (ii) MOLECULE TYPE: DNA (genomic)

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305      (iii) HYPOTHETICAL: NO
307      (vi) ORIGINAL SOURCE:
308          (C) INDIVIDUAL ISOLATE: Human beta-actin gene
311      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
313 GGTGAGTGAG CGGCGCGGGG CCAATCGCGT GCGCCGTTCC GAAAG      45
315 (2) INFORMATION FOR SEQ ID NO: 13:
317      (i) SEQUENCE CHARACTERISTICS:
318          (A) LENGTH: 47 base pairs
319          (B) TYPE: nucleic acid
320          (C) STRANDEDNESS: double
321          (D) TOPOLOGY: linear
323      (ii) MOLECULE TYPE: DNA (genomic)
325      (iii) HYPOTHETICAL: NO
327      (vi) ORIGINAL SOURCE:
328          (C) INDIVIDUAL ISOLATE: Human beta-actin gene
331      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
333 GAGCGGCCGC GCGGCGCCC TATAAAACCC AGCGGCGCGA CGCGCCA      47
335 (2) INFORMATION FOR SEQ ID NO: 14:
337      (i) SEQUENCE CHARACTERISTICS:
338          (A) LENGTH: 50 base pairs
339          (B) TYPE: nucleic acid
340          (C) STRANDEDNESS: double
341          (D) TOPOLOGY: linear
343      (ii) MOLECULE TYPE: DNA (genomic)
345      (iii) HYPOTHETICAL: NO
347      (vi) ORIGINAL SOURCE:
348          (C) INDIVIDUAL ISOLATE: Human cardiac actin gene
351      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
353 TGCTCCAAC TACCCTGTCC ATCAGCGTTC TATAAAGCGG CCCTCCTGGA      50
355 (2) INFORMATION FOR SEQ ID NO: 15:
357      (i) SEQUENCE CHARACTERISTICS:
358          (A) LENGTH: 47 base pairs
359          (B) TYPE: nucleic acid
360          (C) STRANDEDNESS: double
361          (D) TOPOLOGY: linear
363      (ii) MOLECULE TYPE: DNA (genomic)
365      (iii) HYPOTHETICAL: NO
367      (vi) ORIGINAL SOURCE:
368          (C) INDIVIDUAL ISOLATE: Human gene for vascular smooth
369                               muscle alpha-actin
372      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
374 GAGGAGAGCA GGCCAAGGC TATATAACCC TTCAGCTTTC AGCTTCC      47
376 (2) INFORMATION FOR SEQ ID NO: 16:
378      (i) SEQUENCE CHARACTERISTICS:
379          (A) LENGTH: 44 base pairs
380          (B) TYPE: nucleic acid
381          (C) STRANDEDNESS: double
382          (D) TOPOLOGY: linear
384      (ii) MOLECULE TYPE: DNA (genomic)

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/993,346

DATE: 01/30/2002

TIME: 17:24:50

Input Set : N:\Crif3\RULE60\09993346.txt

Output Set: N:\CRF3\01302002\I993346.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:102 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:102 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=2
L:1598 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1598 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=75
L:2672 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:2672 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=127
L:3035 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:3035 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=145
L:3582 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:3582 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=172
L:5705 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:5705 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=275
L:7906 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:7906 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=383
L:7927 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:7927 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=384
L:8948 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:8948 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=434
L:9557 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:9557 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=464
L:10071 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:10071 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=489
L:10092 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:10092 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=490
L:12778 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
L:12778 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=617
L:12854 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=621
L:12874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=622
L:12894 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=623
L:12914 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=624
L:13042 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=630
L:13062 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=631
L:13082 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=632
L:13102 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=633
L:13122 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=634
L:13142 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=635
L:13162 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=636
L:13182 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=637
L:13202 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=638
L:13222 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=639
L:13242 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=640
L:13282 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=642
L:13304 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=643
L:13326 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=644
L:13348 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=645
L:13370 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=646

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L:13392 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=647
L:13414 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=648
L:13436 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=649
L:13458 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=650
L:13480 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=651
L:13502 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=652
L:13524 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=653
L:13546 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=654
L:13568 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=655
L:13590 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=656
L:13612 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=657
L:13634 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=658
L:13656 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=659
L:13680 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=660
L:13703 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=661
L:13726 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=662
L:13749 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=663
L:13789 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:664
L:13792 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:664

US 0999334609P1



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No.	Doccode	Number of pages
1	IDS	3

Total number of pages: 3

Remarks:

Order of re-scan issued on